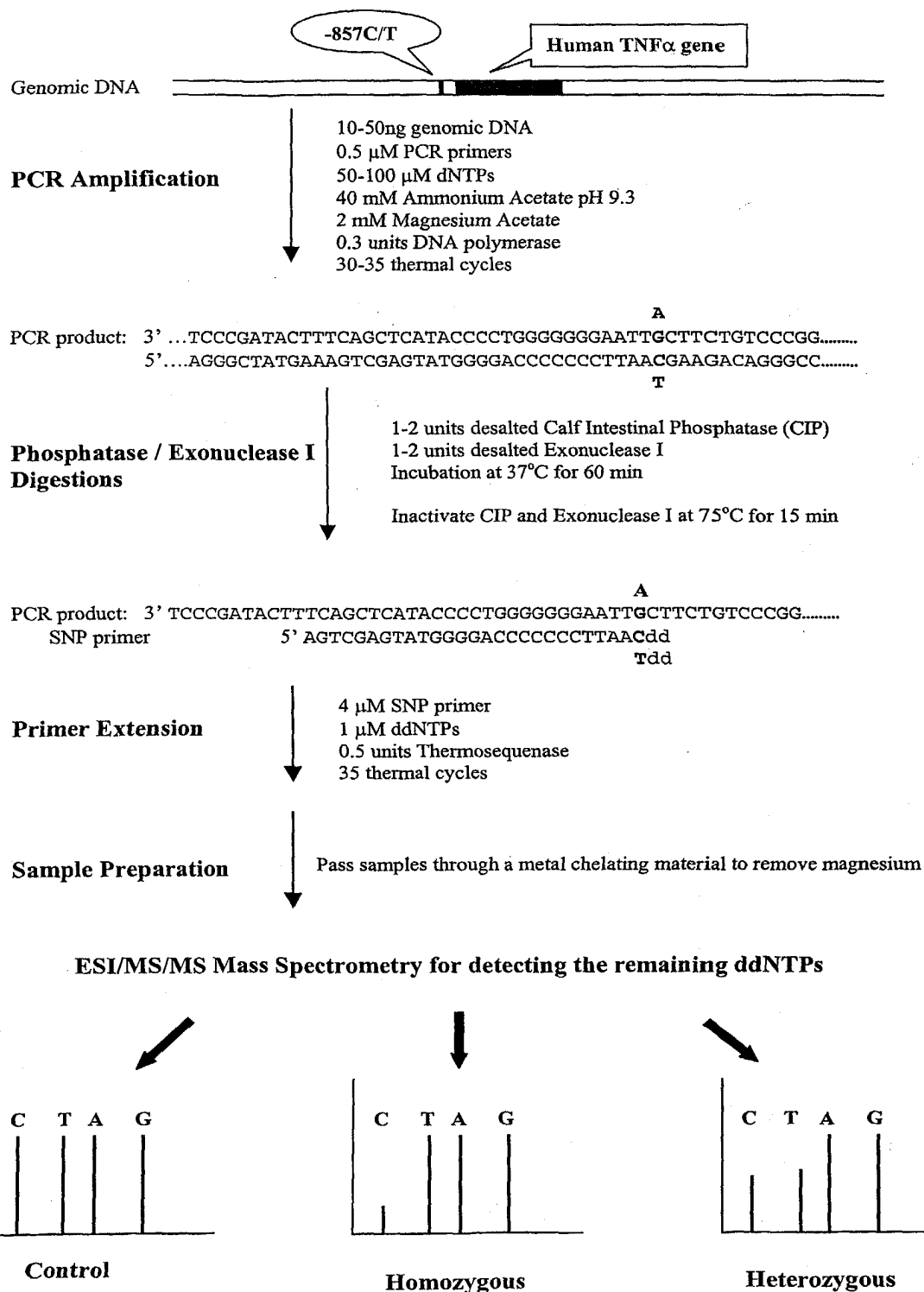
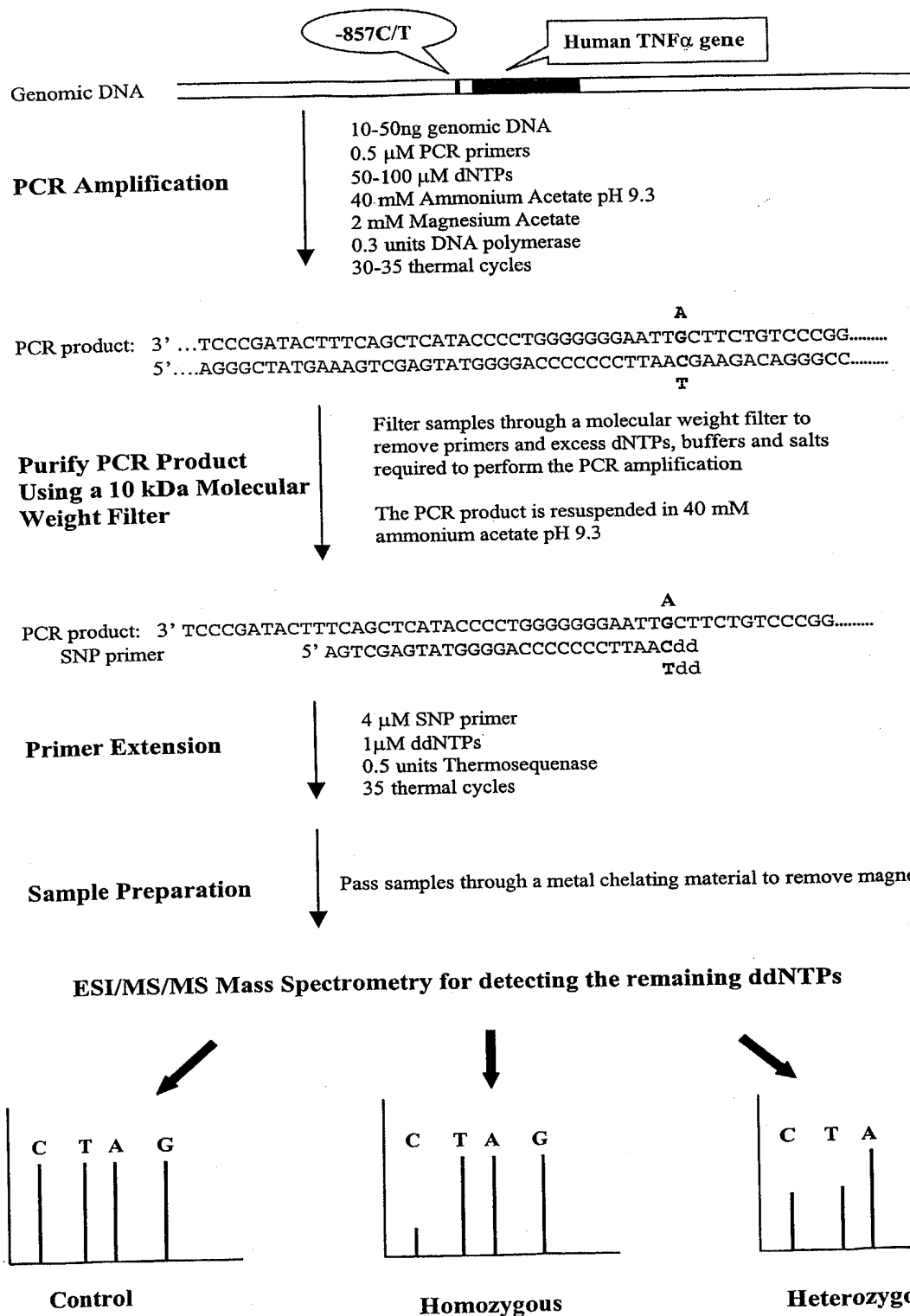


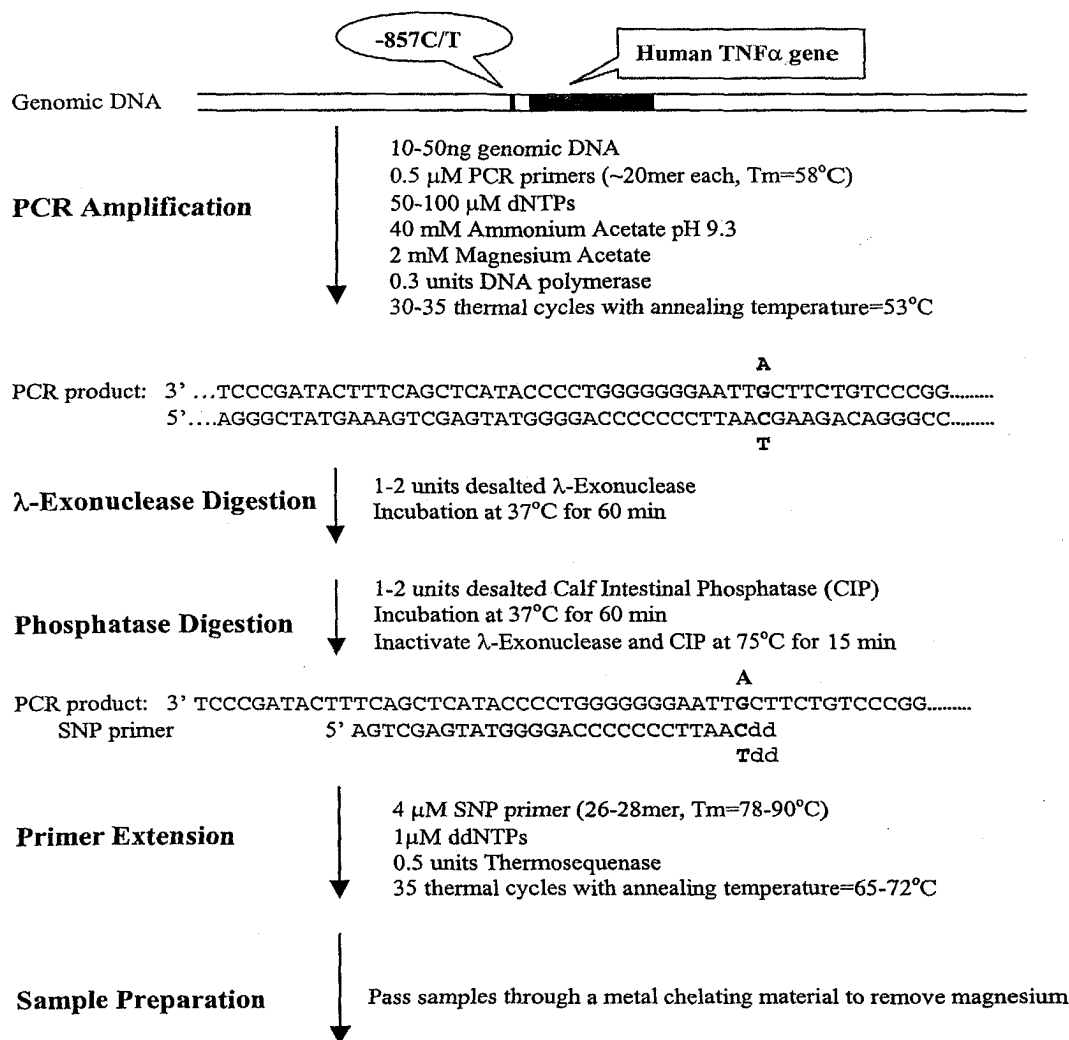
**Figure 1**



### Figure 2



**Figure 3**



ESI/MS/MS Mass Spectrometry for detecting the remaining ddNTPs

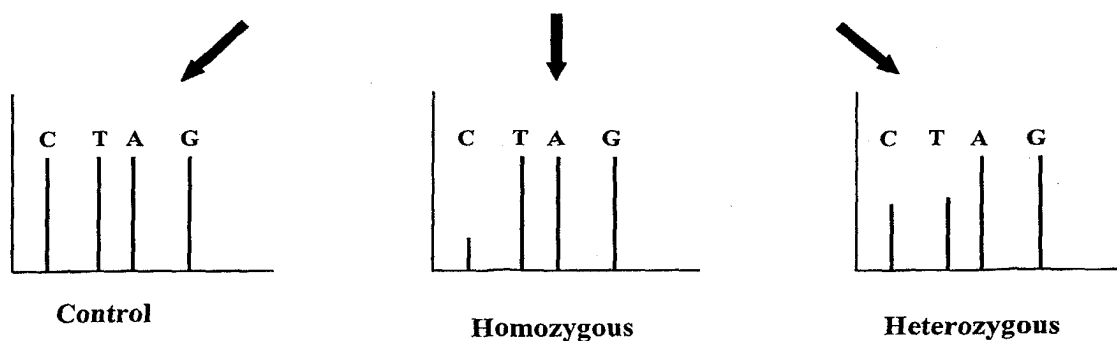
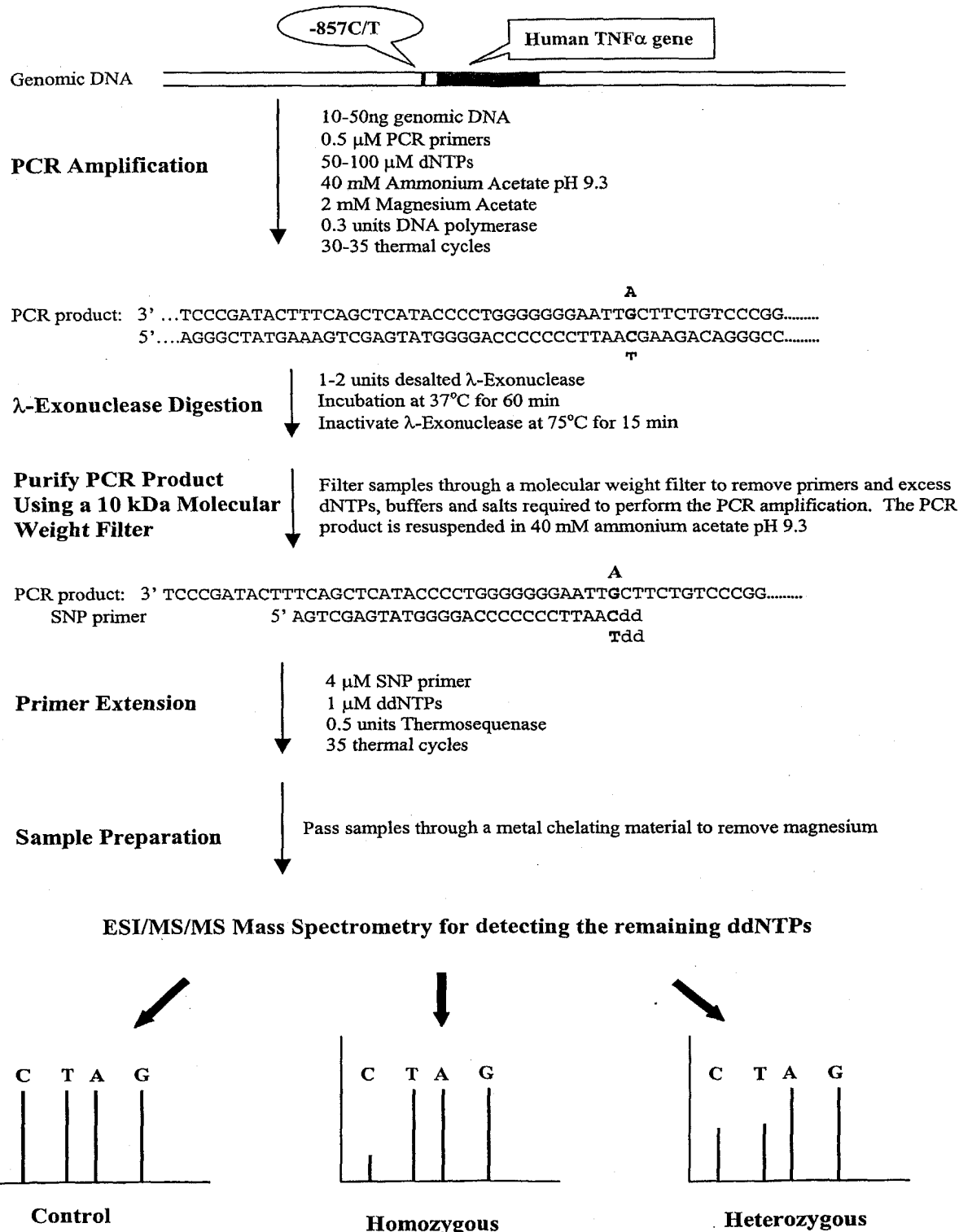
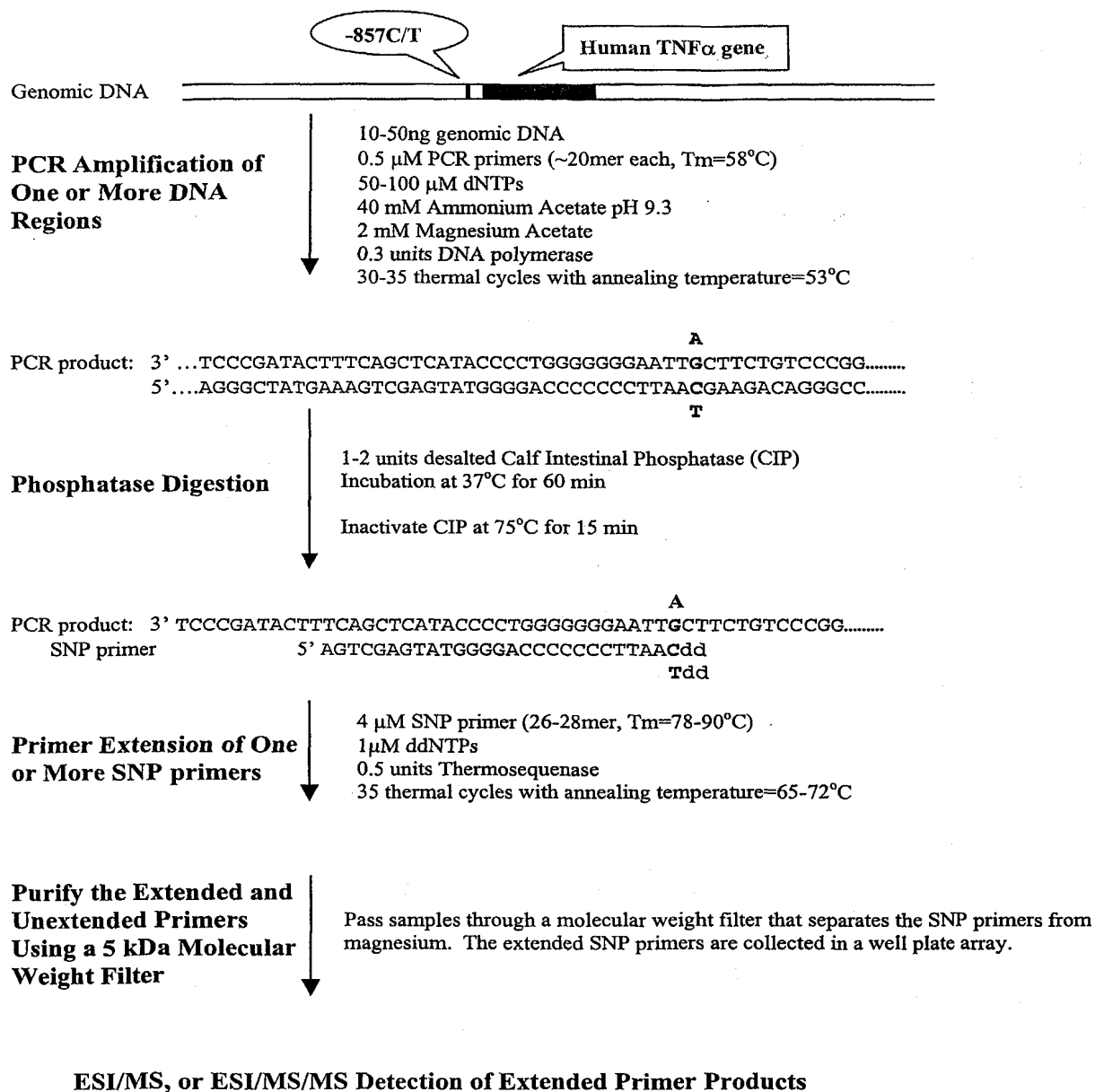


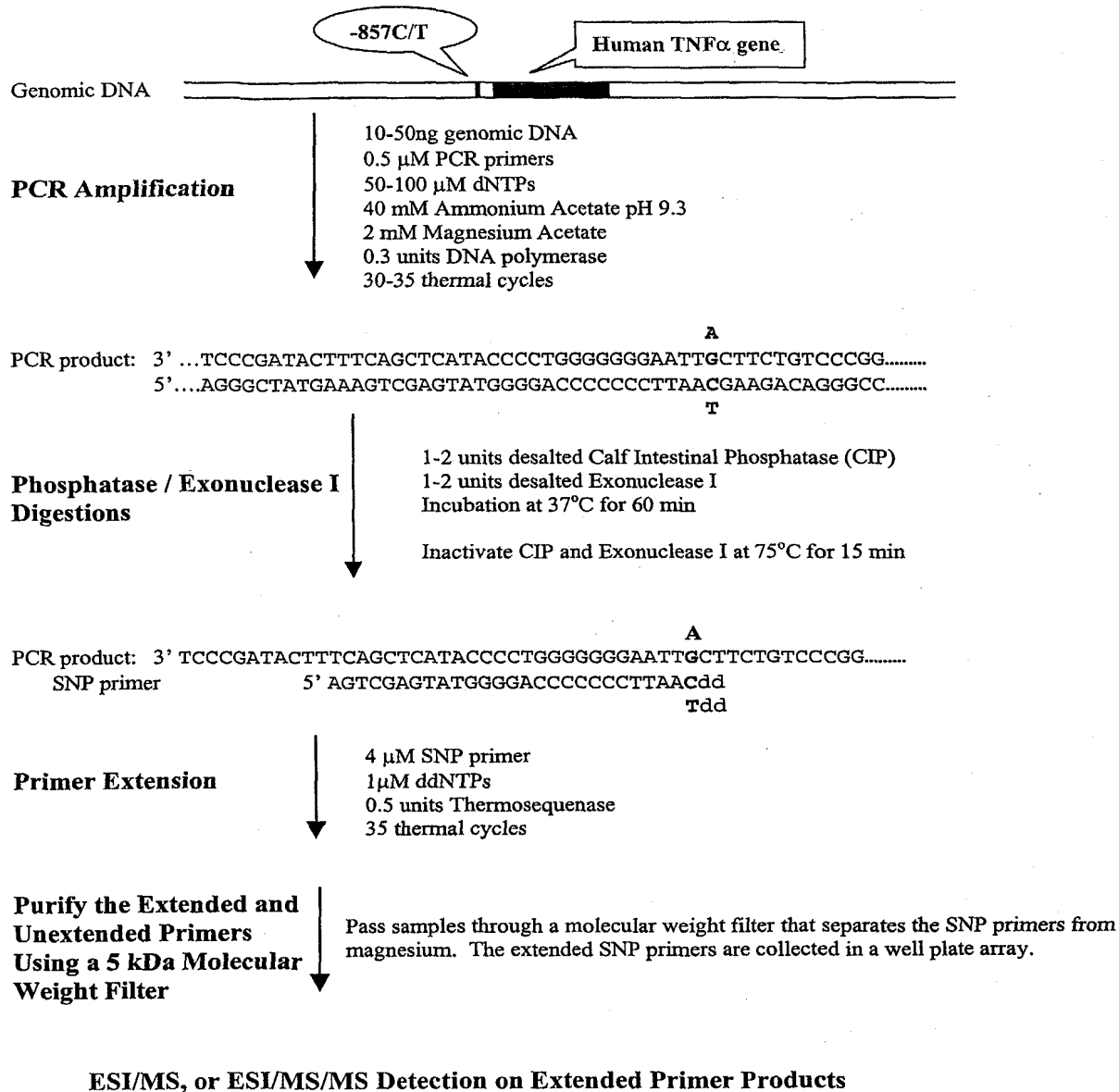
Figure 4



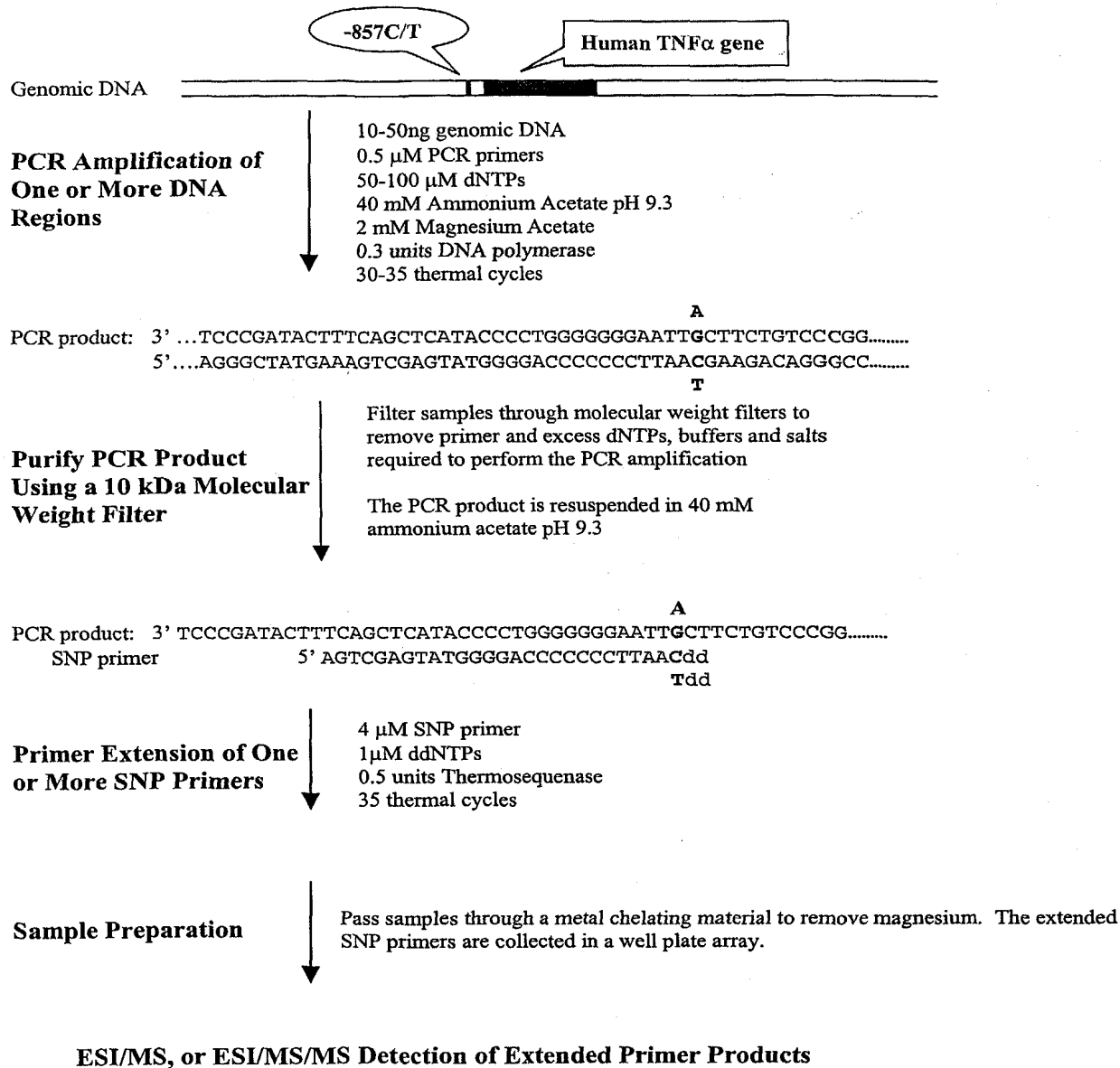
**Figure 5**



**Figure 6**

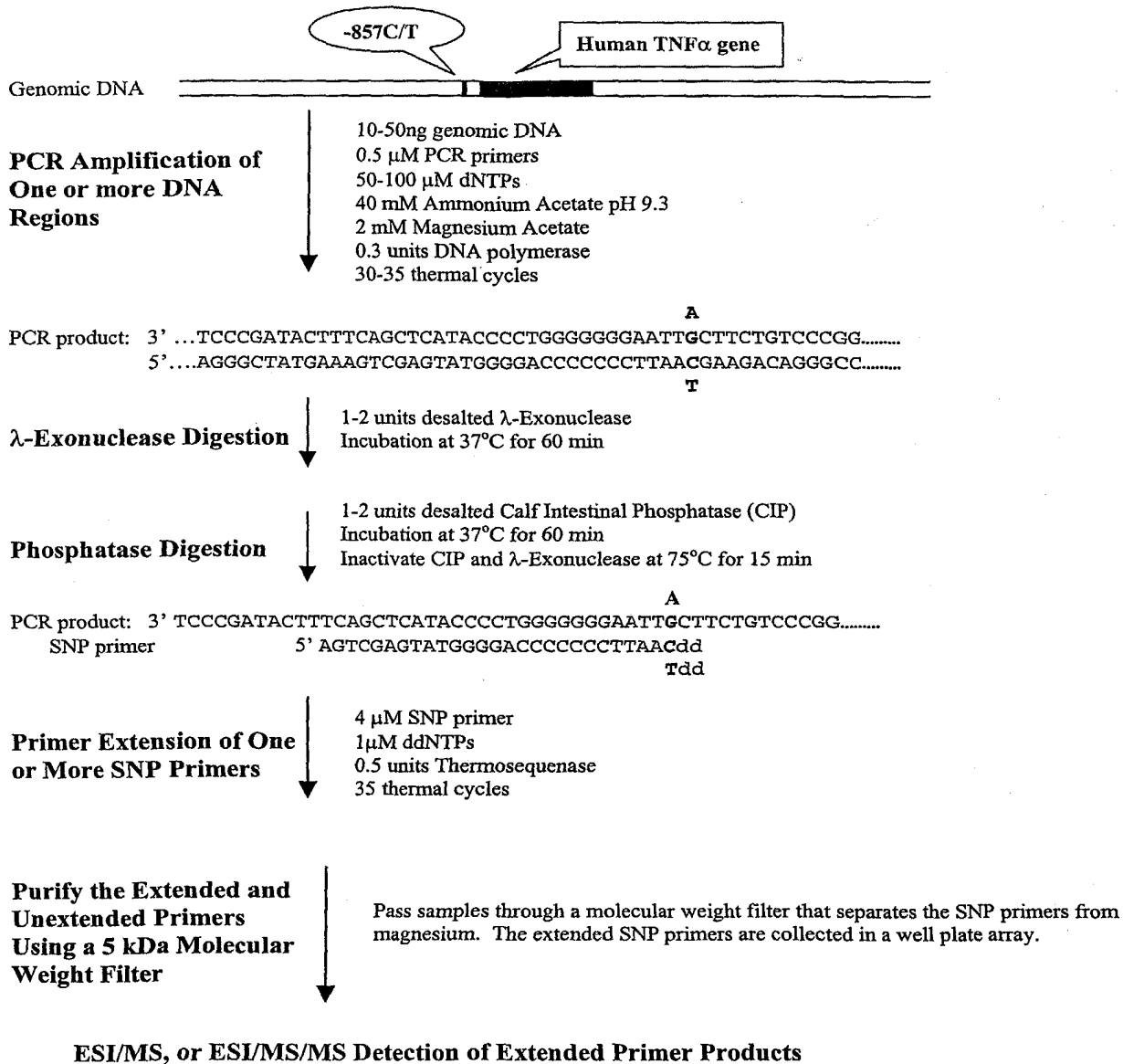


**Figure 7**

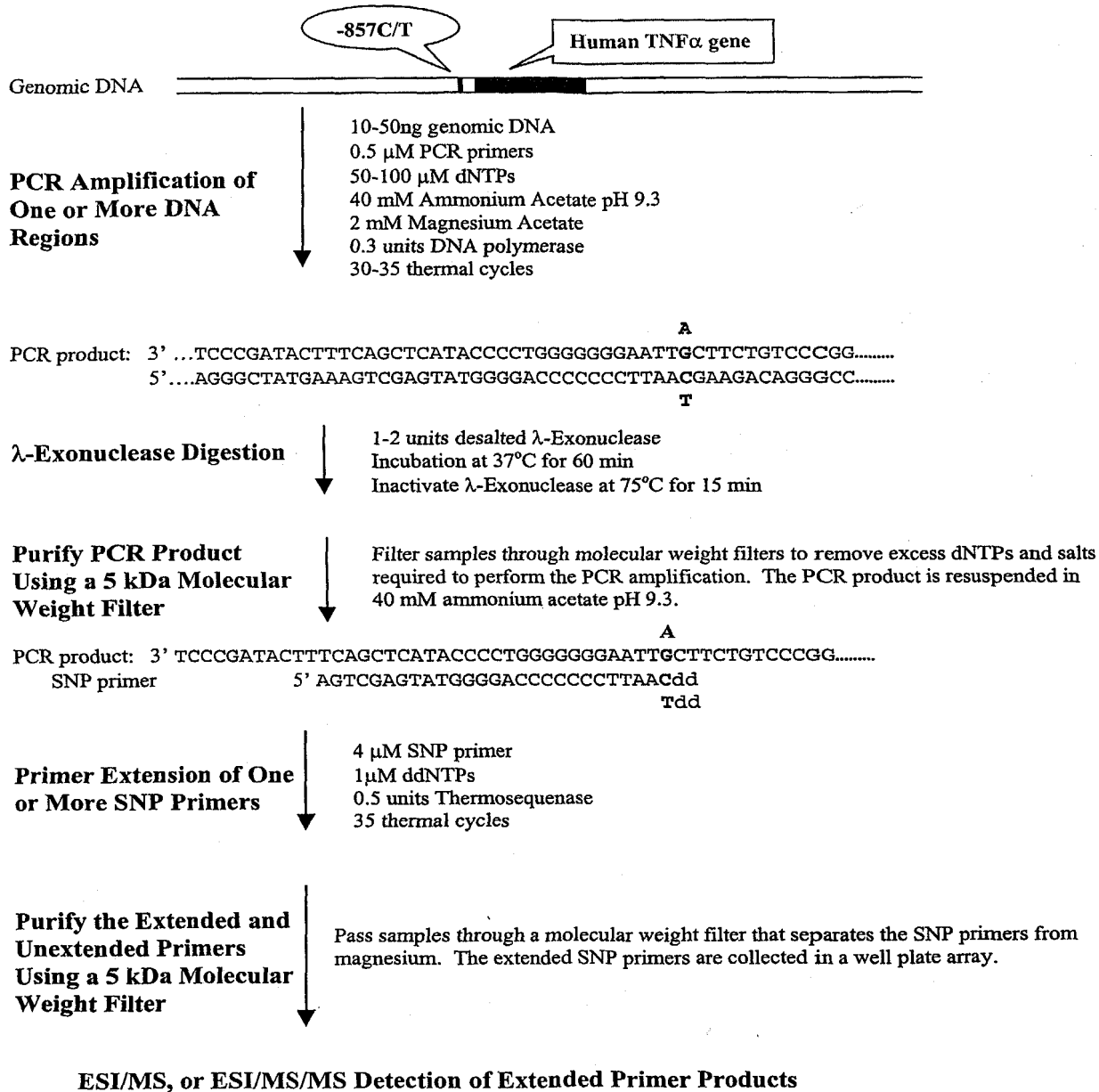


**Figure 8**

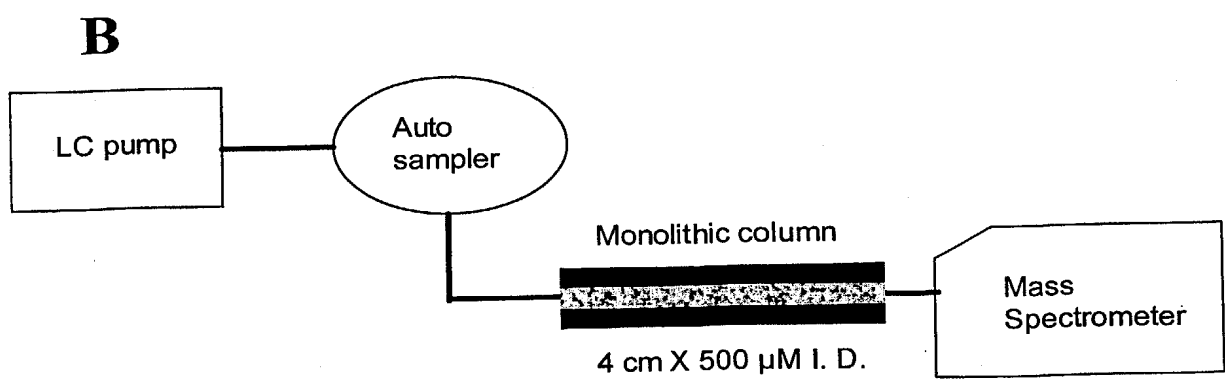
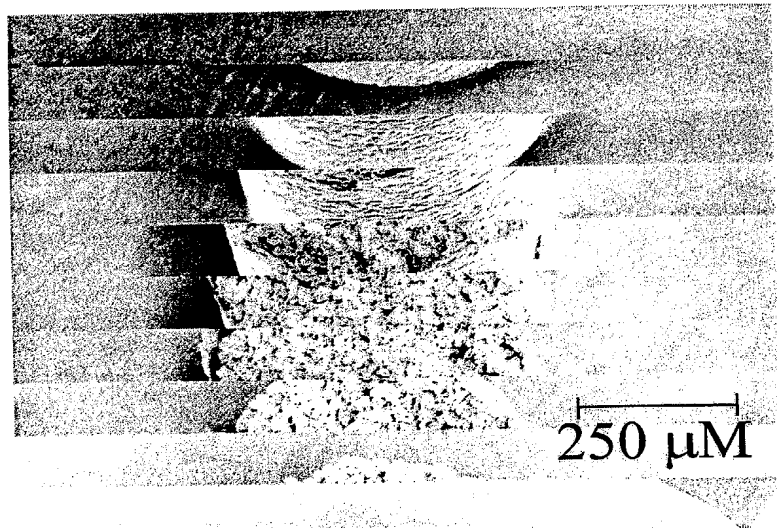




**Figure 9**



**Figure 10**



**Figure 11**

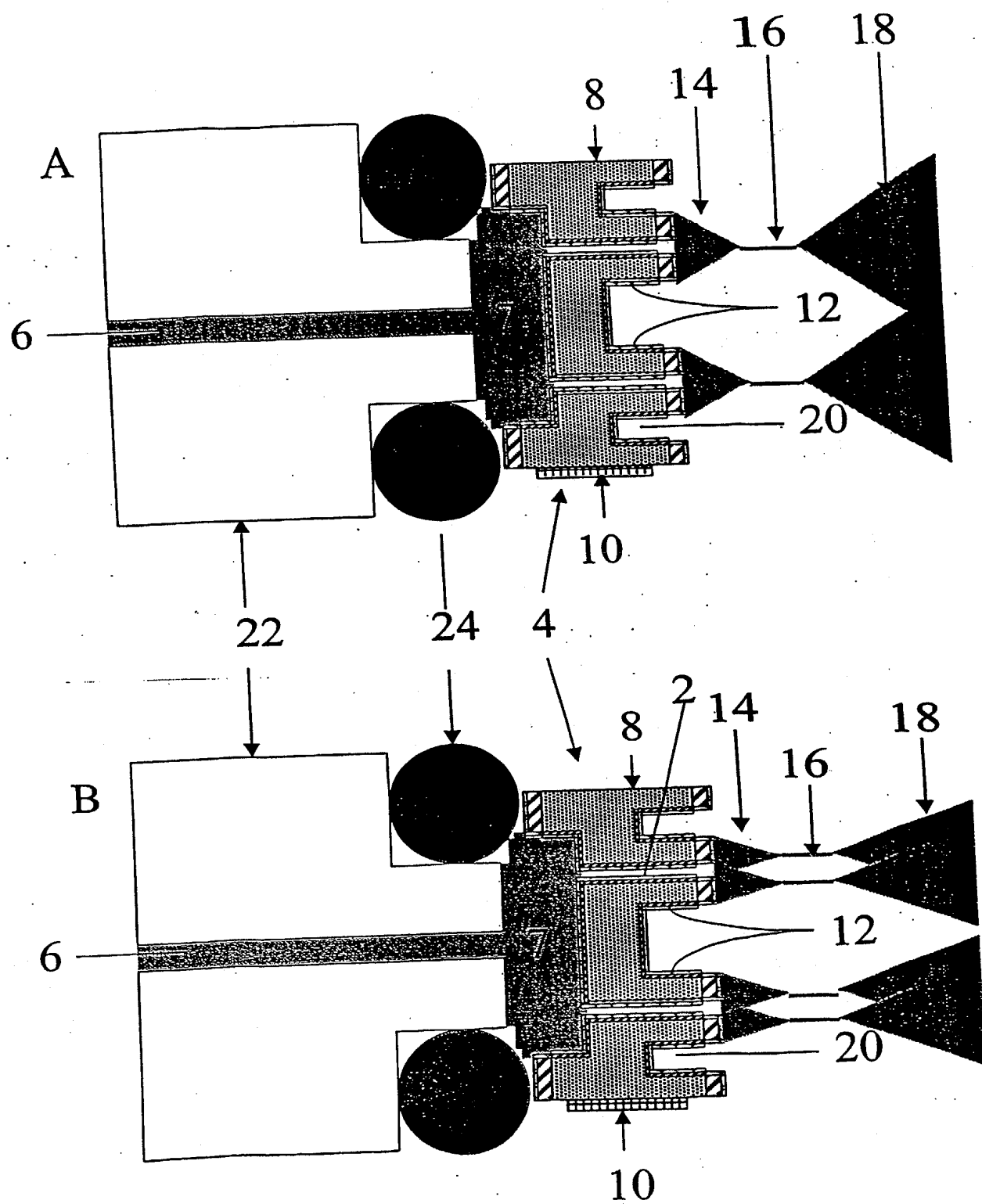


Figure 12

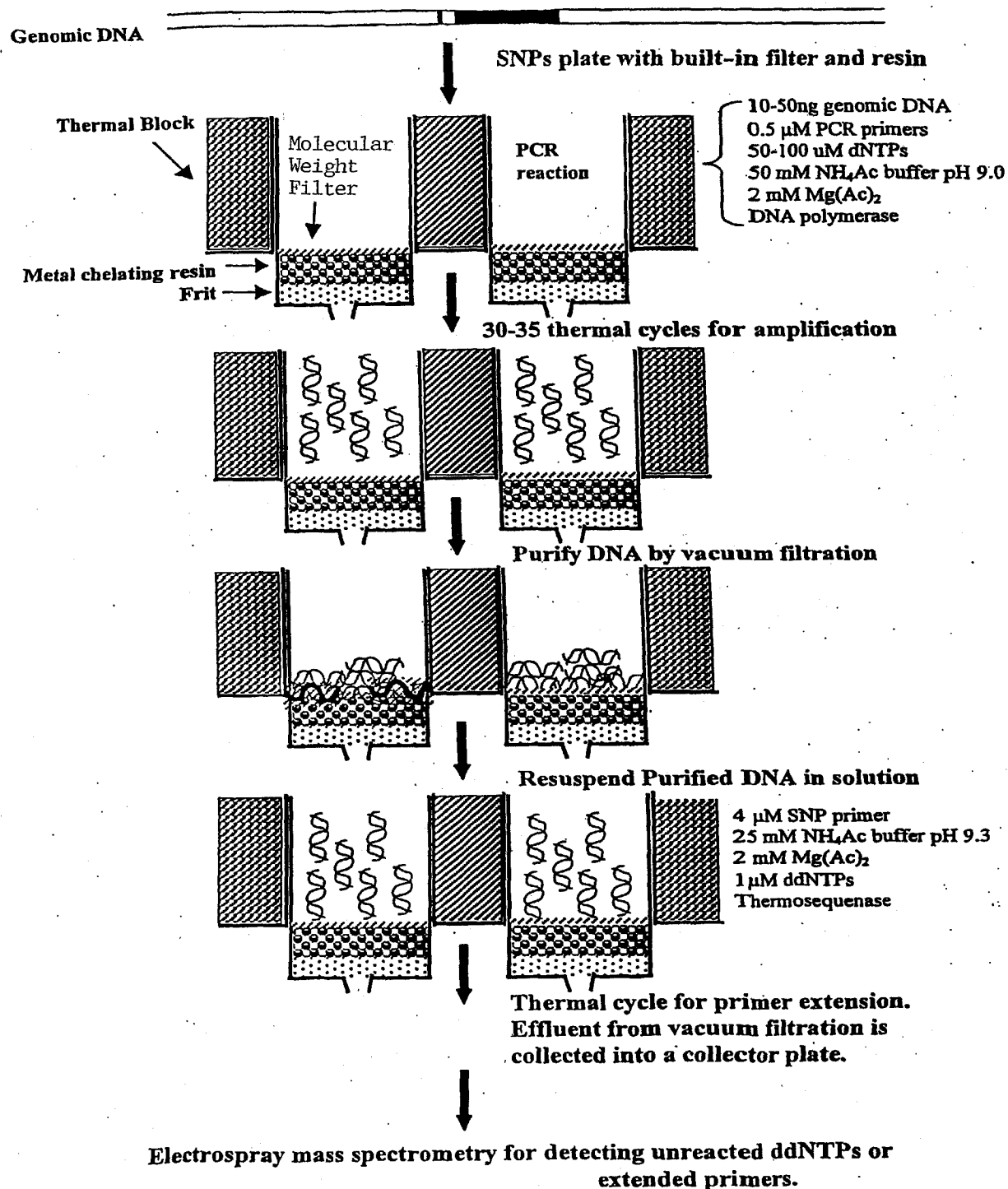


Figure 13

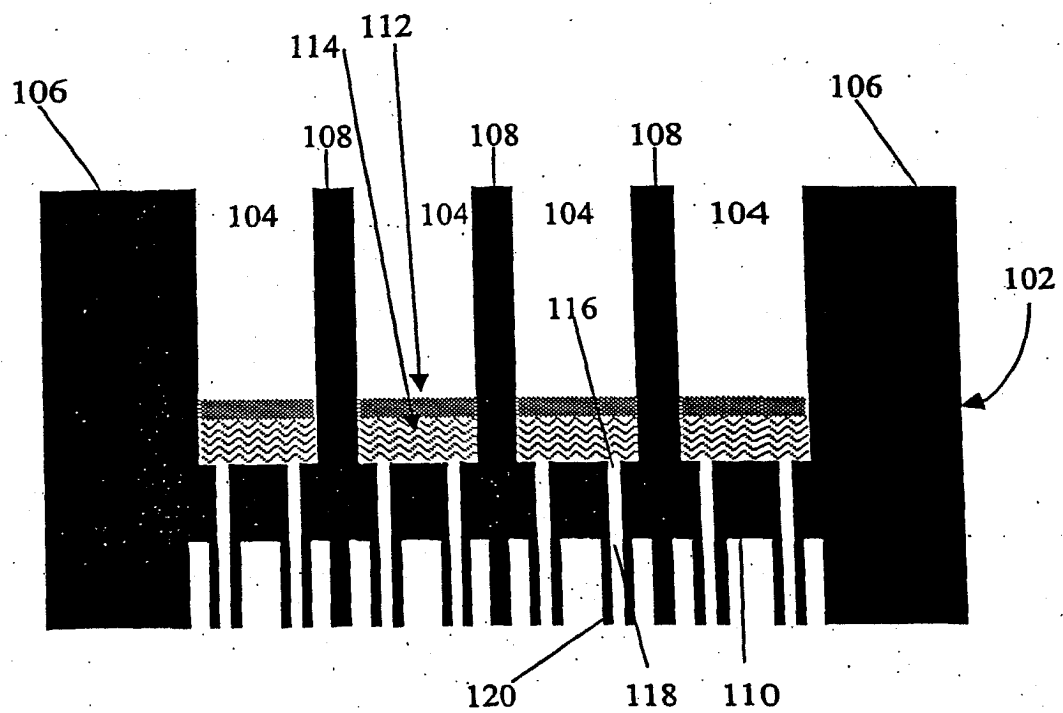
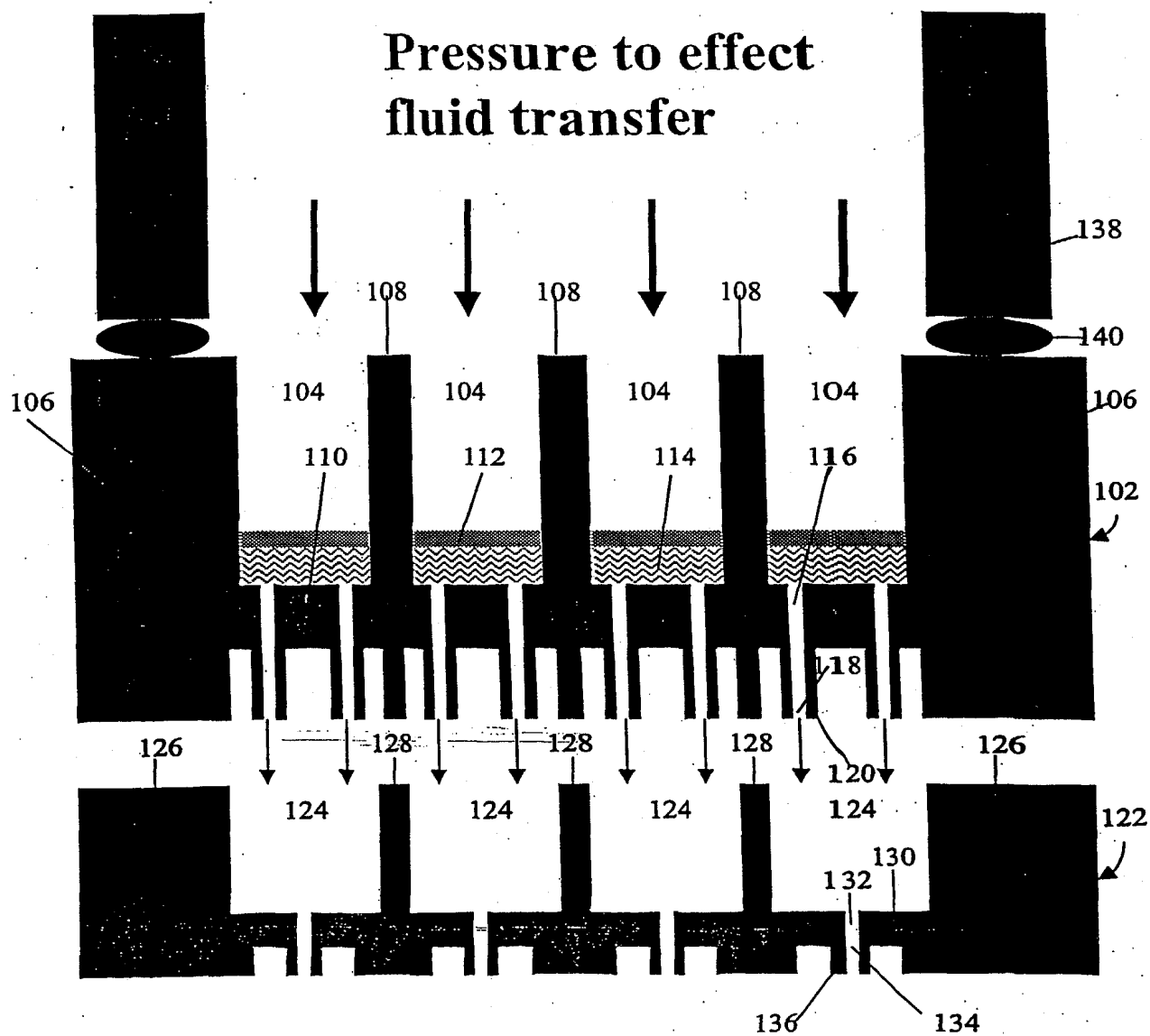


Figure 14A



**Figure 14B**

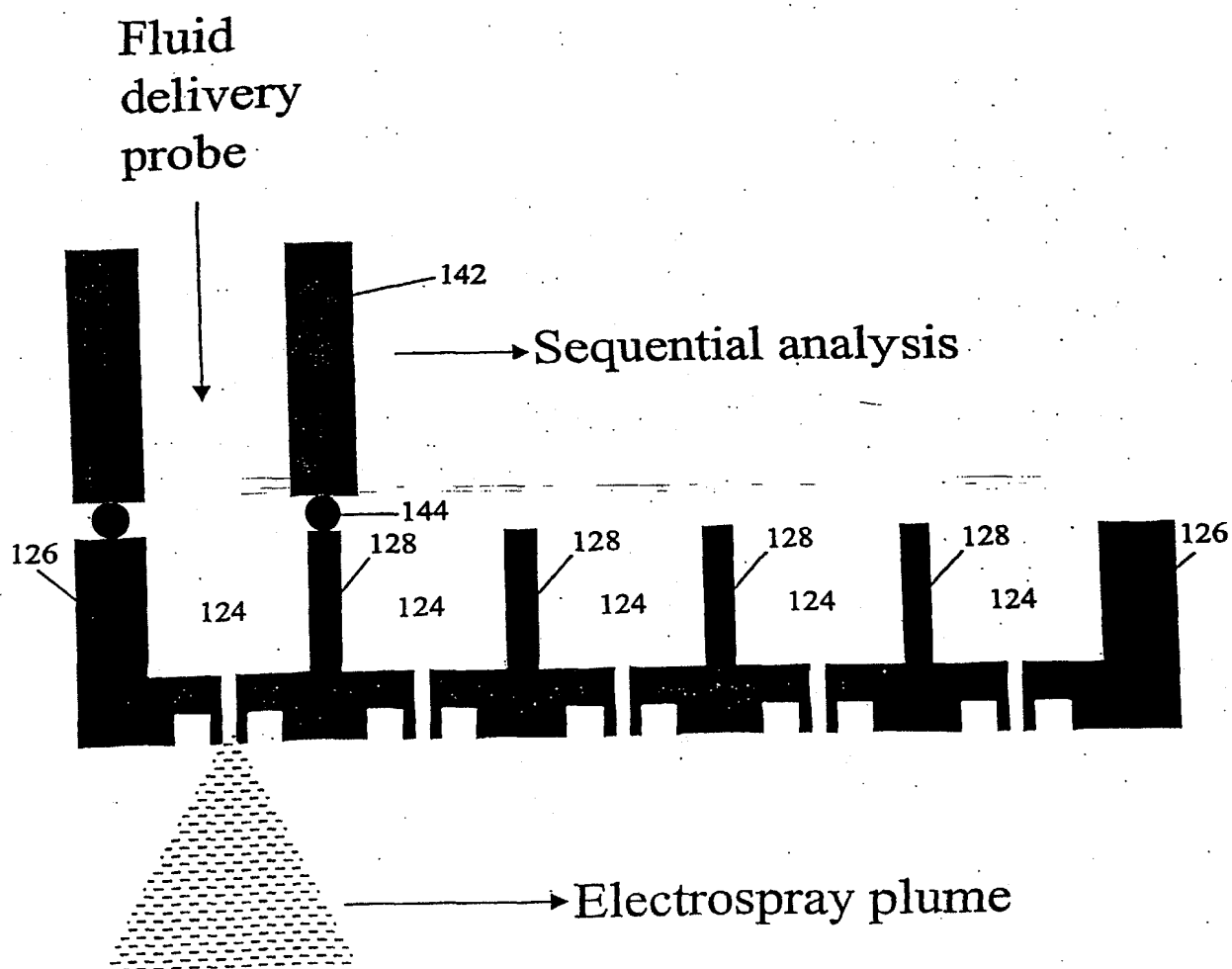


Figure 14C



279bp of Human TNF $\alpha$  promoter DNA (from 3041-3319) (SEQ ID. NO. 1)

857F  
 5'- AAGCAAAGGA GAAGCTGAGA AGATGAAGGA AAAGTCAGGG TCTGGAGGGG  
 3'- TTCGTTTCCT CTTGACTCT TCTACTTCCT TTTCAGTCCC AGACCTCCCC  
 CGGGGGTCAG GGAGCTCCTG GGAGATATGG CCACATGTAG CGGCTCTGAG  
 GCCCCAGTC CCTCGAGGAC CCTCTATACC GGTGTACATC GCCGAGACTC  
 GAATGGGTTA CAGGAGACCT CTGGGGAGAT GTGACCACAG CAATGGGTAG  
 CTTACCCAAT GTCCTCTGGA GACCCCTCTA CACTGGTGTC GTTACCCATC  
 857SNP-forward  
 GAGAATGTCC AGGGCTATGA AAGTCGAGTA TGGGGACCCC CCCTTAACGA  
 CTCTTACAGG TCCCGATACT TTCAGCTCAT ACCCCTGGGG GGGAATTGCT  
 AGACAGGGCC ATGTAGAGGG CCCAGGGAG TGAAAGAGCC TCCAGGACCT  
 TCTGTCCCGG TACATCTCCC GGGGTCCCTC ACTTTCTCGG AGGTCTCTGA  
 CCAGGTATGG AATACAGGGG ACGTTTAAG -3' 3319  
 GGTCCATACC TTATGTCCCC TGCAAATTC -5'  
 857R

Amplification primers:	mer	T <sub>m</sub> (°C)
TNF $\alpha$ -857F 5'- AAGCAAAGGAGAAGCTGAGA-3'	20	58 (SEQ ID. NO. 2)
TNF $\alpha$ -857R 5'- CTAAACGTCCCCTGTATTTC-3'	20	58 (SEQ ID. NO. 3)
SNP primer:		
857SNP-F 5'-AGTCGAGTATGGGGACCCCCCCTTAA-3'	26	82 (SEQ ID. NO. 4)

Figure 15

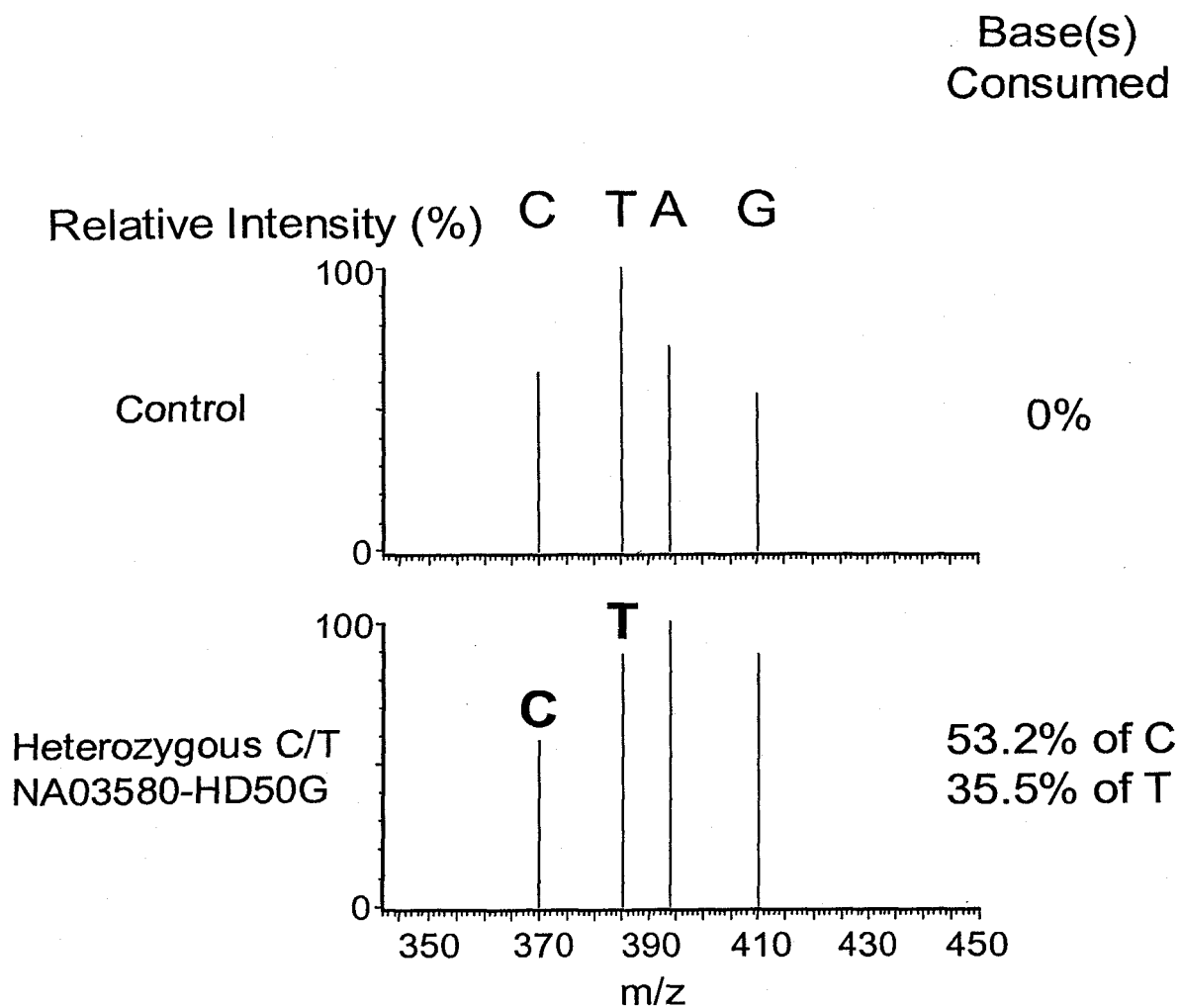


Figure 16

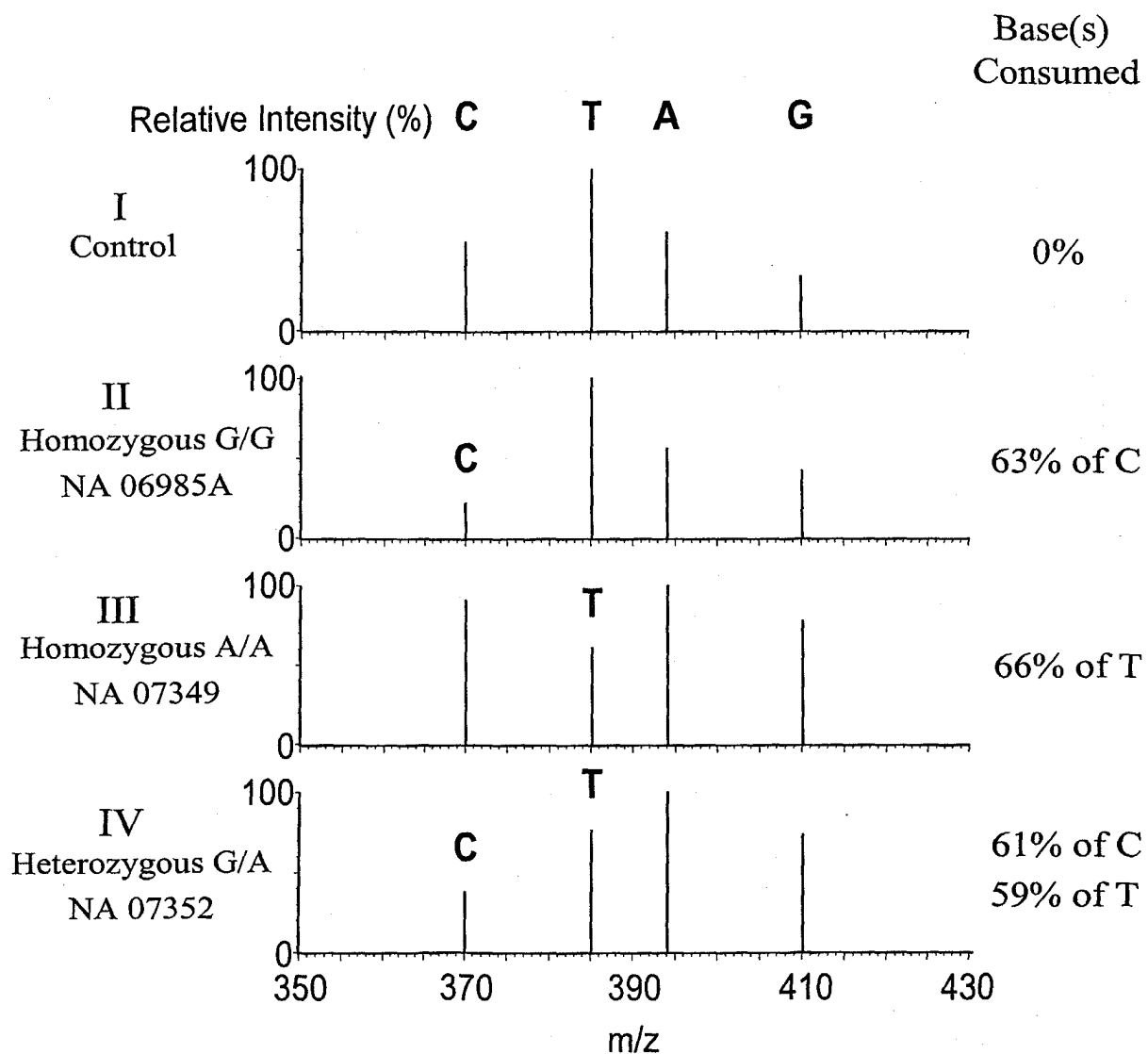
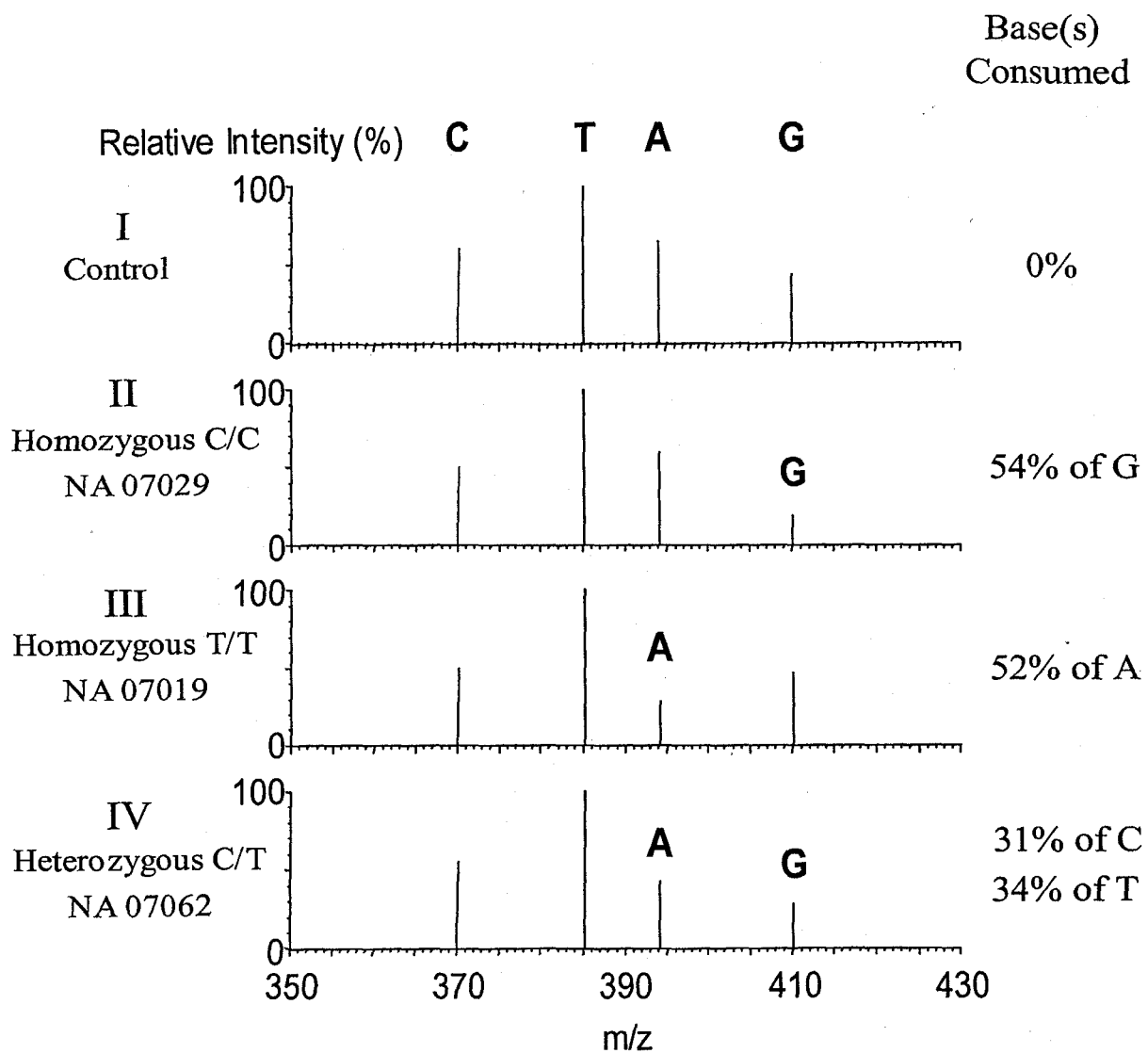
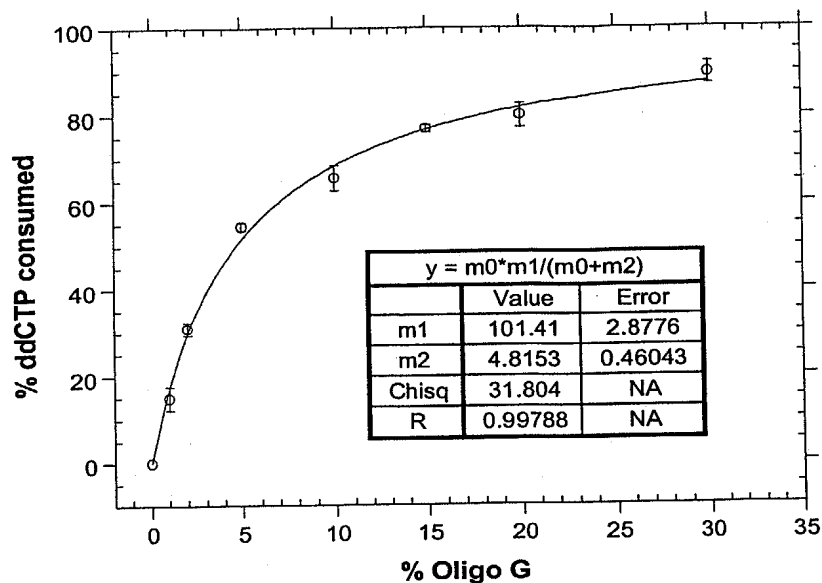


Figure 17



**Figure 18**

(A) Quantitative Pooling Study for Model System



(B) Quantitative Pooling Study for Model System

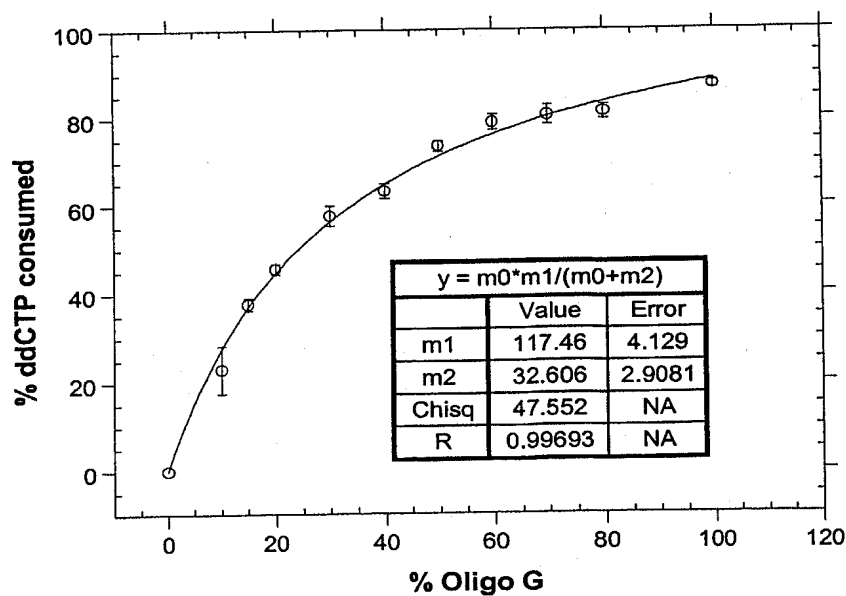
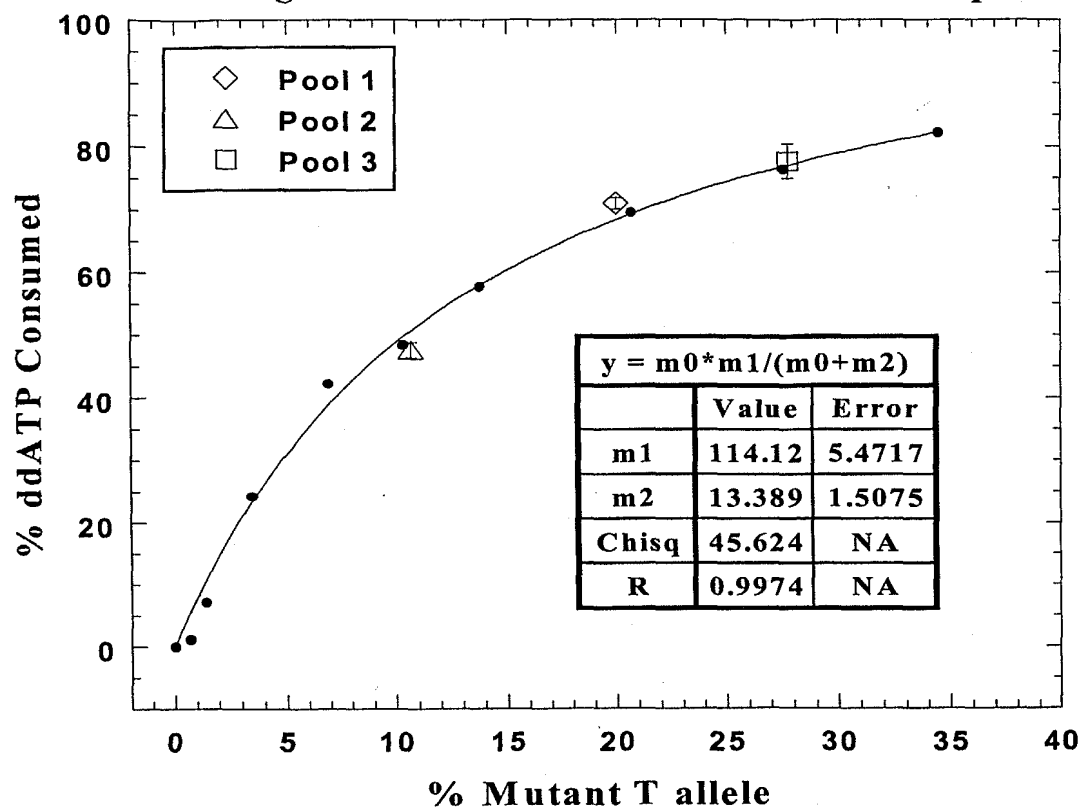


Figure 19

# Quantitative Pooling Study Using Purified Single-Stranded DNA for Region C SNP of Human Genomic Samples



Pooling Sample	Predicted T Allele (%)	Experimental T Allele (%)	Error (%)
Pool 1	20.0	22.0	+10.0
Pool 2	10.7	9.58	-10.5
Pool 3	27.8	28.6	+2.80

Figure 20